

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model  
Run on: February 1, 2005, 13:18:03 ; Search time 28.5 Seconds  
(without alignments)  
2694.605 Million cell updates/sec

Title: US-10-659-782A-11  
Perfect score: 1030  
Sequence: 1 actctggatgggtgctgttt.....tggcagcgaggaggtgggg 579

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 478139 seqs, 66318000 residues  
Total number of hits satisfying chosen parameters: 956278

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters: -MODEL=frame+n2p.model -DEV=xlp  
-Q=/cgn2\_1/USPTO\_spool\_p/US10659782/runat\_01022005\_130353\_14282/app\_query.fasta\_1.775  
-DB=Issued Patents AA -QFMT=fastan -SUFFIX=ra1 -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR\_SCORE=ptc -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFM=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10659782 @CEN\_1.1.46 @runat\_01022005\_130353\_14282 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :				SUMMARIES			
Result No.	Score	Query Match	Length DB ID	Description			
1	326	31.7	117	3	US-09-046-479-2	Sequence 2, Appli	
2	326	31.7	117	3	US-08-822-897C-2	Sequence 2, Appli	
3	326	31.7	117	4	US-09-608-810A-4	Sequence 4, Appli	
4	326	31.7	117	4	US-09-404-417A-2	Sequence 2, Appli	
5	326	31.7	117	4	US-10-140-002-442	Sequence 442, App	
6	117	11.0	181	4	US-09-252-991A-26538	Sequence 26538, A	
7	110.5	10.4	159	4	US-09-252-991A-30696	Sequence 30696, A	
8	110.5	10.7	550	4	US-09-616-289-47	Sequence 47, Appl	
9	109.5	10.6	355	3	US-08-483-533-41	Sequence 41, Appl	
10	109.5	10.6	355	3	US-09-283-471A-41	Sequence 41, Appl	
11	109.5	10.6	355	5	PCT-US91-06532-3	Sequence 3, Appli	
12	108	10.1	174	4	US-09-252-991A-19399	Sequence 19399, A	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

13	107.5	10.4	428	4	US-09-252-991A-24452	Sequence 24452, A	
14	105	9.8	164	4	US-09-252-991A-20615	Sequence 20615, A	
15	105	10.2	409	4	US-09-252-991A-17910	Sequence 17910, A	
16	105	9.8	491	4	US-09-489-039A-7836	Sequence 7836, Ap	
17	103.5	10.0	366	4	US-09-252-991A-17018	Sequence 17018, A	
18	103.5	9.7	427	4	US-09-252-991A-17391	Sequence 17391, A	
19	103	9.7	164	4	US-09-252-991A-30154	Sequence 30154, A	
20	103	9.7	201	4	US-09-252-991A-19786	Sequence 19786, A	
21	103	9.7	355	3	US-08-483-533-41	Sequence 41, Appl	
22	103	9.7	355	3	US-09-283-471A-41	Sequence 3, Appli	
23	103	9.7	355	5	PCT-US91-06532-3	Sequence 43, Appl	
24	103	10.0	538	4	US-09-616-289-43	Sequence 31481, A	
25	102.5	9.6	206	4	US-09-252-991A-31481	Sequence 22335, A	
26	102.5	10.0	299	4	US-09-252-991A-22335	Sequence 18984, A	
27	102	9.9	505	4	US-09-252-991A-18964	Sequence 32877, A	
28	101.5	9.5	249	4	US-09-252-991A-32877	Sequence 19087, A	
29	101.5	9.5	348	4	US-09-252-991A-19087	Sequence 32633, A	
30	101.5	9.9	418	4	US-09-252-991A-32633	Sequence 18234, A	
31	101.5	9.5	1142	4	US-09-252-991A-18234	Sequence 4, Appli	
32	101.5	9.5	1593	3	US-08-628-829-4	Sequence 28157, A	
33	101	9.5	215	4	US-09-252-991A-28157	Sequence 32485, A	
34	100.5	9.4	162	4	US-09-252-991A-32485	Sequence 18853, A	
35	100.5	9.4	1044	4	US-09-252-991A-18853	Sequence 31484, A	
36	99.5	9.7	152	4	US-09-252-991A-31484	Sequence 24671, A	
37	99	9.3	1150	4	US-09-252-991A-24671	Sequence 19862, A	
38	98.5	9.2	217	4	US-09-252-991A-19862	Sequence 31869, A	
39	98.5	9.2	257	4	US-09-252-991A-31869	Sequence 19417, A	
40	98.5	9.6	456	4	US-09-252-991A-19417	Sequence 22704, A	
41	98.5	9.2	587	4	US-09-252-991A-22704	Sequence 23046, A	
42	97.5	9.1	196	4	US-09-252-991A-23046	Sequence 24899, A	
43	97.5	9.1	335	4	US-09-252-991A-24899	Sequence 20649, A	
44	97.5	9.1	575	4	US-09-252-991A-20649	Sequence 27004, A	
45	97.5	9.1	684	4	US-09-252-991A-27004		

ALIGNMENTS

RESULT 1  
US-09-046-479-2  
Sequence 2, Application US/09046479  
Patent No. 6291653  
GENERAL INFORMATION:  
APPLICANT: Sheppard, Paul O.  
APPLICANT: Deisher, Theresa A.  
TITLE OF INVENTION: MOTILIN HOMOLOGS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSER: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/046,479  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sawislak, Deborah A  
REGISTRATION NUMBER: 37,438  
REFERENCE/DOCKET NUMBER: 97-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6672  
TELEFAX: 206-442-6678  
TELEX:

; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 117 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-09-046-479-2

Alignment Scores:  
Pred. No.: 1.57e-25 Length: 117  
Score: 326.00 Matches: 74  
Percent Similarity: 53.19% Conservative: 1  
Best Local Similarity: 52.48% Mismatches: 0  
Query Match: 31.65% Indels: 66  
DB: Gaps: 1

US-10-659-782A-11 (1-579) x US-09-046-479-2 (1-117)

QY 112 ATGCCCTCCCCAGGACCGCTCTGCGCCTCTGCTCTGCGCCTCTGCTGCGCTGCGCTG 171  
Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20  
QY 172 GCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACACAGAGAGTCCAGGTGAGACCTCCC 231  
Db 21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGln--Gln----- 37  
QY 232 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCACACCGCTCTGTGACCTGGAG 291  
Db 37 ----- 37  
QY 292 CAGCAGCGCCATCTCTGGGCTTTCAGTCTTCTCCAGAGACAAAGGACTCTGGGTCTGAC 351  
Db 37 ----- 37  
QY 352 CTCACCTGTTTCTGGAGGACATGGGGCTTAGAGTCTTAACAGACTGTTTCCCCCTTCC 411  
Db 37 ----- 37  
QY 412 AGCAGAGAAAGAGTCCGAAGAAGCCACAGCAAGCTGCAGCCCGAGCTCTAGCAGGCT 471  
Db 38 -----ArgLysGluSerLysProAlaLysLeuGlnProAlaLeuAlaGlyT 56  
QY 472 GGCTCCGCCGGAAGTGGAGGTCAAGCAGAAGGGGCGAGAGGATGAAGTGAAGTCCGG 530  
Db 56 rpLeuArgProGluAspGlyGlnAlaGluGlyAlaGluAspGluLeuGluValArg 75

## RESULT 2

US-08-822-897C-2  
; Sequence 2, Application US/08822897C  
; Patent No. 6380158  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Deisher, Theresa A.  
; TITLE OF INVENTION: MOTILIN HOMOLOGS  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/822,897C  
; FILING DATE:  
; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sawislak, Deborah A  
; REGISTRATION NUMBER: 37,438  
; REFERENCE/DOCKET NUMBER: 97-04  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6672  
; TELEFAX: 206-442-6678  
; TELEX:

; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 117 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-822-897C-2

Alignment Scores:  
Pred. No.: 1.57e-25 Length: 117  
Score: 326.00 Matches: 74  
Percent Similarity: 53.19% Conservative: 1  
Best Local Similarity: 52.48% Mismatches: 0  
Query Match: 31.65% Indels: 66  
DB: Gaps: 1

US-10-659-782A-11 (1-579) x US-08-822-897C-2 (1-117)

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Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20  
QY 172 GCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACACAGAGAGTCCAGGTGAGACCTCCC 231  
Db 21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGln--Gln----- 37  
QY 232 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCACACCGCTCTGTGACCTGGAG 291  
Db 37 ----- 37  
QY 292 CAGCAGCGCCATCTCTGGGCTTTCAGTCTTCTCCAGAGACAAAGGACTCTGGGTCTGAC 351  
Db 37 ----- 37  
QY 352 CTCACCTGTTTCTGGAGGACATGGGGCTTAGAGTCTTAACAGACTGTTTCCCCCTTCC 411  
Db 37 ----- 37  
QY 412 AGCAGAGAAAGAGTCCGAAGAAGCCACAGCAAGCTGCAGCCCGAGCTCTAGCAGGCT 471  
Db 38 -----ArgLysGluSerLysProAlaLysLeuGlnProAlaLeuAlaGlyT 56  
QY 472 GGCTCCGCCGGAAGTGGAGGTCAAGCAGAAGGGGCGAGAGGATGAAGTGAAGTCCGG 530  
Db 56 rpLeuArgProGluAspGlyGlnAlaGluGlyAlaGluAspGluLeuGluValArg 75

## RESULT 3

US-09-608-810A-4  
; Sequence 4, Application US/09608810A  
; Patent No. 6420521  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Jaspers, Stephen R.  
; APPLICANT: Deisher, Theresa A.  
; APPLICANT: Bishop, Paul D.  
; TITLE OF INVENTION: SGIP PEPTIDES  
; FILE REFERENCE: 99-51  
; CURRENT APPLICATION NUMBER: US/09/608,810A  
; FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/141,592

Alignment Scores:		
Pred. No.:	1.57e-25	Length:
Score:	326.00	Matches:
		74
		117

Percent Similarity:	53.19%	Conservative:	1
Best Local Similarity:	52.48%	Mismatches:	0
Query Match:	31.65%	Indels:	66
DB:	4	Gaps:	1

US-10-659-782A-11 (1-579) x US-10-140-002-442 (1-117)

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1	QY	MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu			20
	Db				
172	QY	GCCATGGCAGACTCCAGCTTCCTTGAGCCCTGAACACAGAGAGTCCAGGTGAGACCTCC			231
	Db				
21	QY	AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----			37
	Db				
232	QY	CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACAGCAGCTCTGTGACCTGGAG			291
	Db				
37	QY	-----	-----	-----	37
	Db				
292	QY	CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGCAGCACAAAGCACTCTGGGTCTGAC			351
	Db				
37	QY	-----	-----	-----	37
	Db				
352	QY	CTCACTGTTTCTGGAAGGACATGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCCCTTCC			411
	Db				
37	QY	-----	-----	-----	37
	Db				
412	QY	AGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAAAGCTGCAGGCCCGCAGCTCTAGCAGGCT			471
	Db				
38	QY	-----ArgLysGluSerLysLysProProAlaLysLeuGlnProArgAlaLeuAlaGlyT			56
	Db				
472	QY	GGCTCCCGCCGGAAGATGGAGGTCAACAGAGGGGCGCAGGATGAATCGGAAAGTCCGG			530
	Db				
56	QY	rpLeuArgProGluAspGlyGlyGlnAlaGlyAlaGluAspGluLeuGluValArg			75
	Db				

## RESULT 6

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US-09-252-991A-26538
; Sequence 26538, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26538
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26538

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Alignment Scores:	
Pred. NO.:	0.000927
Score:	117.00
Percent Similarity:	34.62%
Local Similarity:	27.56%
Query Match:	10.97%
DB:	4
Gaps:	8
Indels:	72
Mismatches:	30
Conservative:	11
Matches:	43
Length:	181

US-10-659-782A-11 (1-579) x US-09-252-991A-26538 (1-181)

[illegible]

64	ProGlySerArgAlaGlySer-	----	70
229	GAGGTCTCACTGGACTCTCTGGTGTTCAGGGCTCAGGA-	-----AGC	188
71	-----AlaProAlaGlySerGlyCysArgGlySerGlyArgSerProHisArgAlaAa	88	
187	TGG-----AGCTGCCATGGCCCAAGTCCA	164	
89	TrpLeuArgGlyProAlaSerValHisAspHisGlySerAlaAlaProGlyProAlaPro	108	
163	GCACAGAGATGCCGAGGAGCAGAGGCTGCAGACGGTCCCTGGGGAGG-	-----	116
109	AlaArgArgPheProAlaThrGlyGlyCysArgArgArgGlyGlyArgProGlyGlyCys	128	
115	-----GCATGG-	110	
129	ProLeuHisArgTyrProAlaArgTrpAlaThrAlaGluLeuProAlaTrpArgProLeu	148	
109	---CCTCAGCTGGTGGCAGACAGGTGGGCGCTGCAGTCTCGGCGAGTGGTGGCTGTGCT	53	
149	ProProAlaArgGlyTrpArgThrArgHisArgArgProTrpProThrGly-	165	
52	GTCAGGTCTTATATAGGACAGCGCGTGTGTCTAAACAGCACCCATCCA	5	
166	-----ValArgSerAlaHisPro	171	

## RESULT 7

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US-09-252-991A-30696
; Sequence 30696, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30696
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30696

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Alignment Scores:	
Pred. No.:	0.00417
Score:	110.50
Percent Similarity:	39.31%
Best Local Similarity:	30.64%
Query Match:	10.36%
DB:	4
Gaps:	11
Indels:	5
Mismatches:	51
Conservative:	15
Matches:	53
Length:	159

US-10-659-782A-11 (1-579) x US-09-252-991A-30696 (1-159)

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520 ACTTCATCTCTGCCCCCTCTCTGCTTGACCTCCATCTTCGGGGGGAGCCAGCCTGCTAGA 461
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
7 AlaThrSerArgSerProArgAlaArgProProSerThr--ArgCysSerProAla--Se 25
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::

460 GTCCTGGGCTGCAGCTTGCTGGCTGGCTCTCTCG-----ACTCCTTT 419
      :::  ::::  ::::  ::::  ::::  ::::  ::::  ::::  ::::  ::::
25 rValSerSerAlaAlaAspArgThrSerSerGlyGlnSerProSerThrCysSerProCys 45
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::

418 CTCTCTGTGAAGGGGGAACAGTCTGTTTAGGACTCTAAGCCCCCAGTCTCCTTCAGAAA 359
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
45 sSerSerAla-----AlaProProProCys----- 53

358 CAGTGAGGTTCAGACCCAGACTCTTTTGCTCTGGGAGAAAGACTGAAGCCAGAGATGGC 299
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
54 -SerArgCysSerProAlaArgThrSerCysSerProGlyValAlaSer-----Al 70
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::

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Db 171 gProProArgProProArgGlyCysAlaSerArgProThrSerGlyCysAlaThrTrpTr 191  
 QY 267 -----TAGCAACAGCTCTGTAGCTGAGCAGCAGCGCCATCTCTGGCTTCAG 316  
 Db 191 pSerGlyProArgProProAlaTrpArgAlaAlaAlaArgGlyProAlaSerGly----- 209  
 QY 317 TCTTCTCCAGAGCACAAGGACTCTGGTCT-----GACCTCCTCTGTTCTG 364  
 Db 210 -----ProThrGlyLeuGly-SerGlyAlaGlyTrpArgArgProArgArgSerG 227  
 QY 365 GAAGGACATGGGGCTTAGAGCTCTAAACAGAGCTGTTTCCCTCCCTCCAGCAGAGAAGGA 424  
 Db 227 lyArgAlaTrpGlyProArgProValProGlyProTrpProAlaGluProAlaArgArgT 247  
 QY 425 GTCCAGAGAGCCACAGCCAGCTGCA-----GCCCGAGCTCTAGC 466  
 Db 247 hrArgSerAsnValThrProGlu-AlaAlaTrpValPheArgGlyAlaProGlySerSer 266  
 QY 467 -----AGGCTGGCTCCCGCGAGATGAGGTCAAGCAGA----- 502  
 Db 267 AlaProSerArgSerProGluArgArgTrpGlnGluProArgIleTyrThrLeuGlyAla 286  
 QY 503 -----AGGGCAGAGGATGAATGCTGAAGTCCGGTCCG 535  
 Db 287 SerProProSerGlnGlyProProArgGlyArgAsp----- 299  
 QY 536 TACCTCTGCAGTTTATGCTCTGTGG-----CAGCAGAGAGGG 574  
 Db 300 -----TrpProIleGlyGlyArgGlnArgGlyGly 309

RESULT 11  
 PCT-US91-06532-3  
 ; Sequence 3, Application PC/TUS9106532  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Roizman, Bernard  
 ; TITLE OF INVENTION: Recombinant Herpes Simplex Viruses  
 ; TITLE OF INVENTION: Vaccines and Methods  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSES: Marshall, O'Toole, Gerstein, Murray &  
 ; ADDRESSES: Bicknell  
 ; CITY: Chicago  
 ; STREET: Two First National Plaza Suite 2100  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60603  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US91/06532  
 ; FILING DATE: 19910910  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Gruber, Lewis S.  
 ; REGISTRATION NUMBER: 30,060  
 ; REFERENCE/DOCKET NUMBER: 27373/8235  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312/346-5750  
 ; TELEFAX: 312/984-9740  
 ; TELEX: 25-3856  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 355 amino acids  
 ; TYPE: AMINO ACID  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 PCT-US91-06532-3

Alignment Scores: 0.00725 Length: 355  
 Pred. No.:

Score: 109.50 Matches: 66  
 Percent Similarity: 33.75% Conservative: 15  
 Best Local Similarity: 27.50% Mismatches: 73  
 Query Match: 10.63% Indels: 86  
 DB: 5 Gaps: 13

US-10-659-782A-11 (1-579) x PCT-US91-06532-3 (1-355)

QY 44 AGACCTGACAGCAGCAGCAGCAGCAGCTCCGCCAGGACTGCGAGGCCAC----- 88  
 Db 95 ArgProThrAlaAlaAlaProArgProGly-----ProHisArgProAlaTrpAla 112  
 QY 89 CTGTCTGCAACCCAGCTGAGGCATGCTCCCTCCAGGACCTCTGCA----- 136  
 Db 113 ArgGlyAlaGlyLeuThrProProThrProProArgAlaProSerAlaPheArgAla 132  
 QY 137 -----GCTCTCTGCTCTCG-----GCATGCTCTGCTCG 166  
 Db 133 SerProSerAlaCysAlaSerProArgSerThrTrpArgAlaCysAlaCysAsp-Ala 152  
 QY 167 ACTTGCCATGCGAGGCTCCAGCTTCTGAGCCCTGAACACAGCAGAGAGTCCAGGTGAGAC 226  
 Db 152 gAlaGlyArgGlyArgSerProProArgProProArgProProArgPro---ProAr 171  
 QY 227 CTCCCCCAAGCCCAACATGTTTCCAGCCCTGCCACT----- 266  
 Db 171 gProProArgProProArgGlyCysAlaSerArgProThrSerGlyCysAlaThrTrpTr 191  
 QY 267 -----TAGCAACAGCTCTGTGACCTGAGCAGCAGCGCCATCTCTGGCTTCAG 316  
 Db 191 pSerGlyProArgProProAlaTrpArgAlaAlaAlaArgGlyProAlaSerGly----- 209  
 QY 317 TCTTCTCCAGCAGCAAAAGGACTCTGGTCT-----GACCTCCTCTGTTCTG 364  
 Db 210 -----ProThrGlyLeuGly-SerGlyAlaGlyTrpArgArgProArgArgSerSerG 227  
 QY 365 GAAGGACATGGGGCTTAGAGCTCTAAACAGAGCTTTCCTCCCTCCAGCAGAGAAGGA 424  
 Db 227 lyArgAlaTrpGlyProArgProValProGlyProTrpProAlaGluProAlaArgArgT 247  
 QY 425 GTCCAGAGAGCCACAGCAGCAAGCTCA-----GCCCGAGCTCTAGC 466  
 Db 247 hrArgSerAsnValThrProGlu-AlaAlaTrpValPheArgGlyAlaProGlySerSer 266  
 QY 467 -----AGGCTGGCTCCCGCGAGATGAGGTCAAGCAGA----- 502  
 Db 267 AlaProSerArgSerProGluArgArgTrpGlnGluProArgIleTyrThrLeuGlyAla 286  
 QY 503 -----AGGGCAGAGGATGAATGCTGAAGTCCGGTCCG 535  
 Db 287 SerProProSerGlnGlyProProArgGlyArgAsp----- 299  
 QY 536 TACCTCTGCAGTTTATGCTCTGTGG-----CAGCAGAGAGGG 574  
 Db 300 -----TrpProIleGlyGlyArgGlnArgGlyGly 309

RESULT 12  
 US-09-252-991A-19399  
 ; Sequence 19399, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 19399

```
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19399

Alignment Scores:
Pred. No.: 0.00785 Length: 174
Score: 108.00 Matches: 48
Percent Similarity: 34.86% Conservative: 13
Best Local Similarity: 27.43% Mismatches: 66
Query Match: 10.12% Indels: 48
DB: 4 Gaps: 9

US-10-659-782A-11 (1-579) x US-09-252-991A-19399 (1-174)
QY 577 CCACCTCTCGTGGCCACAGACATAAACTCCAGAGGTACCGACCGGACTTCCAGT 518
Db 11 ProProSer-----ArgAArgSerGlyProAlaProValPro---ArgAlaProGly 26
QY 517 TCATCCTCTGCCCTCTGCTTGCATCTCCATCTTCCGGCGGAGCCAGCTGTAGAGT 458
Db 27 SerAlaGlySerProArgAla---SerProGlyGlyCysArgIleProProArgArg 45
QY 457 CGGGCTGCAGCTTGGCTGGTCTTCTCGACTCTTCTCGTGGAGGGGAAACA 398
Db 46 ArgGlySerSer-----SerPro 51
QY 397 GTCTGTTTAGGACTCTAAGCCCATGTCTTCCAGAAACAGTGAGTCCAGACCCAGAGT 338
Db 52 ValArgProGlyArgProGlyHisLeuArgArgAlaArgArgAlaProArgPro 71
QY 337 CTTTGTCTCTGGGAGAGAGTGAAGCCAGAGATGGCGCTGCTGCTCCAGGTACAGA 278
Db 72 SerArgCysSerGlySerGlySerArgProArgSerGlyArgSerAlaProGlySerArg 91
QY 277 GCTGTTGCTAAGTGGCAGGCTGGACACATGTGGGCTTTGTGG---GAGGTCTCA 221
Db 92 -----ArgThrProArgCysAlaProProProSer 101
QY 220 CTGGAGTCTCTGTTGAGGCTCAGGAAGCTGG-----AGCTGCTCCATGGCCAAGT 167
Db 102 Pro-----GlyArgArgArgTrpArgSerThrThrProGlyProGly 115
QY 166 CCAGCCAGATCCCGAGGAGCAGGAGGCTGCAGCGTCCCTG-----122
Db 116 SerArgArgLeuThrAlaGlyArgProGlyCysArgArgAspTrpProValA-gThrGly 135
QY 121 -----GGGAGGCGATGGCTCAGCTGGTTGCAGA 92
Db 136 LysArgArgArgProGlyArgSerHisProProValGlyCysArg 150

RESULT 13
US-09-252-991A-24452
; Sequence 24452, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24452
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24452

Alignment Scores:
Pred. No.: 0.0157 Length: 164
Score: 105.00 Matches: 51
Percent Similarity: 32.99% Conservative: 14
Best Local Similarity: 25.89% Mismatches: 68
```

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Alignment Scores:
Pred. No.: 0.0126 Length: 428
Score: 107.50 Matches: 49
Percent Similarity: 36.42% Conservative: 14
Best Local Similarity: 28.32% Mismatches: 70
Query Match: 10.44% Indels: 40
DB: 4 Gaps: 8

US-10-659-782A-11 (1-579) x US-09-252-991A-24452 (1-428)
QY 44 AGACCTGACAGACACAGGACACCACTCCGACAGAGTGCAGGCCACCTGTCTGCAACCCAG 103
Db 175 ArgAlaAspArgProGlyThrTyralaProGly-----ArgProGlnArg 189
QY 104 CTGAGCCATGCCCTCCCGAGGACCTCTCGAGCCCTGACGAGAGTCCAGGTGA 223
Db 190 LeuArgProLeuProSerAlaGlyProSerArg-----201
QY 164 TGGACTTGGCCATGGCAGGCTCCAGCTTCCAGCCCTGACGAGAGTCCAGGTGA 223
Db 202 TrpArgLeu-HisGlyArgLeuLeuProGlnGlnCysArgHisArgHisProGlyVa 221
QY 224 GACCTCCCA-----CAAAGCCCCACATGTTGTTCCAGCCCTGCACTTA 268
Db 221 lProArgProGlyCysProAlaArgGlyAspProArgCysArgLeuSerProTrpGlnAr 241
QY 269 GCAACACAGCTCTGTGACCTGGAGCAGCAGCCCATCTCTGGGCTTCCAGTCTTCCAGCA 328
Db 241 gHisPro-----GlyTyrlleuLeuProAr 250
QY 329 GCACAAGAGCTCTGGTCTGACCTGACCTTCTGGAAGGACATGGGGCTTAGAGTCC 388
Db 250 gArgCysAlaValArgLeuAspPro-----TrpArgSerAlaGly 263
QY 389 TAAACAGAGCTGTTCCCTTCCAGCAGAGAGAGTGAAGAGCCACCCAGCAAGCT 448
Db 264 -ArglleProValLeuProArgLeuArgArgAlaArgArgArgArgGlyLe 283
QY 449 GCAGCCCGAGCTGTAGCAGGC---TGGCTCCGC-----CCGGAAGATGAGGTCAAGC 499
Db 283 uGlnProGlnLeuSerAlaGlyProTrpGlnArgLeuGlyProLeuValGlyGlyAlaAr 303
QY 500 AGAAGGGGAGGAGTGAAGTCCGAACTCCGGGTCGT 536
Db 303 gArgArgLeuArgAlaAspArgArgLeuArgProGly 315

RESULT 14
US-09-252-991A-20615
; Sequence 20615, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20615
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20615

Alignment Scores:
Pred. No.: 0.0157 Length: 164
Score: 105.00 Matches: 51
Percent Similarity: 32.99% Conservative: 14
Best Local Similarity: 25.89% Mismatches: 68
```



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Query Match: 9.84% Indels: 64
DB: Gaps: 10
US-10-659-782A-11 (1-579) x US-09-252-991A-20615 (1-164)
QY 574 CCTCTCTGCTCCACAGAGCATAAACTGCAGAGGTACCCAGCGGACTTCCAGTTCA 515
DB 1111111111111111111111111111111111111111111111111111111
7 ProGlySerThrProSerArg-----ValProSerArgThrSerArgSer 21
QY 514 TCCTCTGCCCCCT-----503
DB 22 AlaSerArgProCysArgSerIleAlaAlaThrTpsrThrAlaAlaArgProMetPro 41
QY 502 ---TCTGCTTGACCTCCATCTTCCGGGGGAGCCAGCTGTAGAGCTCGGGGCTGCAGC 446
DB 42 AnSerAlaGlyProIleArgSerGlySerArgAlaMetArgArgAlaThrSer 61
QY 445 TTGGCTGGTGGCTTCTTCTGCTCTGGAAGGGGAAACAGTCTGTTTAGGA 386
DB 62 CysAla-----ThrTrpAlaGly-----67
QY 385 CTCTAAGCCCCCATGCTCTTCCAGAAACAGTGAGGTACAGCCAGAGTCTTTGTCTCT 326
DB 68 -----ThrProArgPro-----71
QY 325 GGGAGAGACTGAGCCAGAGATGGCGCTGCTGCTCCAGGTCCAGAGCTGGTGTCTMA 266
DB 72 GlyArgArgMetProArg-----ArgSerGlyProAlaThrArgCysCysSer 89
QY 265 GTGGCAGGCGCTGAA-----CAACATGTGGGGCTTGTGGGGAGGTCTCACCTGGACTC 212
DB 90 ThrThrSerCysArgCysCysAlaAlaThrThrSerSerAlaGlySerIleSerValArgPro 109
QY 211 TCTGTGTGTGAGGGTTCAGGAAGCTGGAGCTGCCATGCCCAAGTCCAGCCAGAGATGC 152
DB 110 ThrGly---ArgGlySerAlaSer-----AlaProAlaArgSerThr 122
QY 151 CGAGGAGCAGGAGGTCTGAGACGGTCCCTGGGGAGGCGATGGCTCAGCTGGGTGCAGA 92
DB 123 AlaProMetTrpArgCysTrpProArgCysSerThrArgTrpProAlaAlaArgSerAlaArg 142
QY 91 CAGGTGGGCTGCAGTCC---TGGGGAGTGGTGGCTGTGCTGCTCAGGTCT 44
DB 143 ArgSerAlaAlaThrSerCysTrpArgSerAlaSerAlaSerThrArgAla 159

RESULT 15
US-09-252-991A-17910
; Sequence 17910, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17910
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17910

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Alignment Scores:
Pred. No.: 0.0225 Length: 409
Score: 105.00 Matches: 54
Percent Similarity: 34.88% Conservative: 21
Best Local Similarity: 25.12% Mismatches: 52
Query Match: 10.19% Indels: 88

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DB: 4 Gaps: 10
US-10-659-782A-11 (1-579) x US-09-252-991A-17910 (1-409)
QY 117 CTCCCGAGGACCGTCTGCAGCTCTCTCGGCATGCTCTCGCTGAGTCTGGCTGACCTGGCCAT 176
DB 1111111111111111111111111111111111111111111111111111111
194 IleSerArgSerHisCysSerSerProProArgThrSerArgSerGlyMetGly--- 212
QY 177 GGCAGGCTCCAGTCTCTGAGCCCTGAACACCAGAGATCCAGGTGAGACCTCCCCACAA 236
DB 213 -----ArgSerGlnGlyThrGlnArgGlySer 221
QY 237 AGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAAC-----CAGCTCTGTGACCTGA 290
DB 1111111111111111111111111111111111111111111111111111111
222 SerProAlaSerCysSerIleArgAlaArg-SerSerGlyCysArgAlaCysSerAlaSe 241
QY 291 GCAGCAGCGCCATCTC-----306
DB 241 rArgProArgArgArgSerSerMetAspAsnArgProTrpThrArgThrArgGluIleTh 261
QY 307 -----TGGGCT---TCAGTCTTCTCCAGAGACACAAAGGACTCTGGGTC 347
DB 261 rPheSerAlaGluAenTrpSerLeuSerGlnTrpGlnArgSerThrAlaAspSerGlyAr 281
QY 348 TGACCTCACT-----GTTTCTGGAAGGACATGGGGCTTAGAGTCTTAACAG 395
DB 281 gArgIleSerAlaIlelleArgLeuLeuGlyArgSerValProValArgSerAlaGlyAr 301
QY 396 ACTGTTTCCCTC-----TCCAGCAGAGAAAGGAGTCCGAAGAAGCCACAGCCAG 446
DB 301 gArgPheAlaProGluArgSerGlySerArgAspArgGlyArgArg-CysValAlaAspA 321
QY 447 CT-----GCAGCCCGAGCTCTAGCAGGCTGGCTCGG-----478
DB 321 laProThrAlaArgCysGlySerAlaProAlaArgSerArgProSerProTrpArgGlyA 341
QY 479 -----CCCGGA- 484
DB 341 rgAspGlyGlySerArgArgArgAlaGlyArgLeuAlaGlyArgArgTrpTrpProGlys 361
QY 485 -----AGATGGAGGTCAAGCAGAGAGGGGCGAGAGGATGAACCT- 520
DB 361 erGlyProAlaProArgArgLeuArgTrpArgTrpArgArgProGlyArgGlyTrpSerA 381
QY 521 -----GGAAGTCCGGTCCG 535
DB 381 laSerAspAlaArgHisArgArgAlaGlySerProGlyArg 394

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Job time : 31.5 secs

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